

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/587,804
Source: 1FWP
Date Processed by STIC: 8/8/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/587,804

TIME: 09:07:30

Input Set : A:\0279woSEQ.ST25.txt

Output Set: N:\CRF4\08082006\J587804.raw

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3 <110> APPLICANT: Maxygen Holdings Ltd.
4     Maxygen ApS
5     Bouquin, Thomas
7 <120> TITLE OF INVENTION: Regulated Stop Codon Readthrough
9 <130> FILE REFERENCE: 0279wo310
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/587,804
C--> 12 <141> CURRENT FILING DATE: 2006-07-31
14 <150> PRIOR APPLICATION NUMBER: US 60/540,820
15 <151> PRIOR FILING DATE: 2004-01-30
17 <150> PRIOR APPLICATION NUMBER: US 60/631,306
18 <151> PRIOR FILING DATE: 2004-11-29
20 <160> NUMBER OF SEQ ID NOS: 27
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1524
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial
29 <220> FEATURE:
30 <223> OTHER INFORMATION: PC-GPI cassette
33 <220> FEATURE:
34 <221> NAME/KEY: exon
35 <222> LOCATION: (1)..(1518)
37 <400> SEQUENCE: 1
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39 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
40 1             5             10             15
42 tcc ggc aca cca gct cct ctt gac tca gtg ttc tcc agc agc gag cgt      96
43 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
44             20             25             30
46 gcc cac cag gtg ctg cgc atc cgc aaa cgt gcc aac tcc ttc ctg gag      144
47 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
48             35             40             45
50 gag ctc cgt cac agc agc ctg gag cgg gag tgc ata gag gag atc tgt      192
51 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
52 50             55             60
54 gac ttc gag gag gcc aag gaa att ttc caa aat gtg gat gac aca ctg      240
55 Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
56 65             70             75             80
58 gcc ttc tgg tcc aag cac gtc gac ggt gac cag tgc ttg gtc ttg ccc      288
59 Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
60             85             90             95
62 ttg gag cac ccg tgc gcc agc ctg tgc tgc ggg cac ggc acg tgc atc      336
63 Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile

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64		100		105		110		
66	gac ggc atc ggc agc ttc agc tgc gac tgc cgc agc ggc tgg gag ggc							384
67	Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly							
68		115		120		125		
70	cgc ttc tgc cag cgc gag gtg agc ttc ctc aat tgc tgc ctg gac aac							432
71	Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn							
72		130		135		140		
74	ggc ggc tgc acg cat tac tgc cta gag gag gtg ggc tgg cgg cgc tgt							480
75	Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys							
76	145		150		155		160	
78	agc tgt gcg cct ggc tac aag ctg ggg gac gac ctc ctg cag tgt cac							528
79	Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His							
80		165		170		175		
82	ccc gca gtg aag ttc cct tgt ggg agg ccc tgg aag cgg atg gag aag							576
83	Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys							
84		180		185		190		
86	aag cgc agt cac ctg aaa cga gac aca gaa gac caa gaa gac caa gta							624
87	Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val							
88		195		200		205		
90	gat ccg cgg ctc att gat ggg aag atg acc agg cgg gga gac agc ccc							672
91	Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro							
92		210		215		220		
94	tgg cag gtg gtc ctg ctg gac tca aag aag aag ctg gcc tgc ggg gca							720
95	Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala							
96	225		230		235		240	
98	gtg ctc atc cac ccc tcc tgg gtg ctg aca gcg gcc cac tgc atg gat							768
99	Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp							
100		245		250		255		
102	gag tcc aag aag ctc ctt gtc agg ctt gga gag tat gac ctg cgg cgc							816
103	Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg							
104		260		265		270		
106	tgg gag aag tgg gag ctg gac ctg gac atc aag gag gtc ttc gtc cac							864
107	Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His							
108		275		280		285		
110	ccc aac tac agc aag agc acc acc gac aat gac atc gca ctg ctg cac							912
111	Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His							
112		290		295		300		
114	ctg gcc cag ccc gcc acc ctc tcg cag acc ata gtg ccc atc tgc ctc							960
115	Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu							
116	305		310		315		320	
118	ccg gac agc ggc ctt gca gag cgc gag ctc aat cag gcc ggc cag gag							1008
119	Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu							
120		325		330		335		
122	acc ctc gtg acg ggc tgg gga tat cac agc agc cga gag aag gag gcc							1056
123	Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala							
124		340		345		350		
126	aag aga aac cgc acc ttc gtc ctc aac ttc atc aag att ccc gtg gtc							1104
127	Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val							
128		355		360		365		

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130 ccg cac aat gag tgc agc gag gtc atg agc aac atg gtg tct gag aac      1152
131 Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
132      370                      375                      380
134 atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc      1200
135 Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
136 385                      390                      395                      400
138 gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg      1248
139 Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
140      405                      410                      415
142 gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac      1296
143 Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
144      420                      425                      430
146 ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg att cat ggg cac      1344
147 Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
148      435                      440                      445
150 atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct ctg gaa ccc      1392
151 Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro Leu Glu Pro
152      450                      455                      460
154 acg tac tgc gac ctc gcc cct ccc gct ggc acg acc gat gcc gct cac      1440
155 Thr Tyr Cys Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala His
156 465                      470                      475                      480
158 cct ggc cgg agc gtc gtg cct gcc ctc ctg cct ctg ctc gcc ggg acc      1488
159 Pro Gly Arg Ser Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr
160      485                      490                      495
162 ctc ctg ctc ctg gaa acc gct acc gct ccc tagtaa      1524
163 Leu Leu Leu Leu Glu Thr Ala Thr Ala Pro
164      500                      505
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 1533
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial
172 <220> FEATURE:
173 <223> OTHER INFORMATION: PC-UAAC-GPI-4Stop cassette
176 <220> FEATURE:
177 <221> NAME/KEY: exon
178 <222> LOCATION: (1)..(1521)
179 <223> OTHER INFORMATION: 1384-1386: TAA stop codon
181 <400> SEQUENCE: 2
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183 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
184 1                      5                      10                      15
186 tcc ggc aca cca gct cct ctt gac tca gtg ttc tcc agc agc gag cgt      96
187 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
188      20                      25                      30
190 gcc cac cag gtg ctg cgc atc cgc aaa cgt gcc aac tcc ttc ctg gag      144
191 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
192      35                      40                      45
194 gag ctc cgt cac agc agc ctg gag cgg gag tgc ata gag gag atc tgt      192
195 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys

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196	50		55		60												
198	gac	ttc	gag	gag	gcc	aag	gaa	att	ttc	caa	aat	gtg	gat	gac	aca	ctg	240
199	Asp	Phe	Glu	Glu	Ala	Lys	Glu	Ile	Phe	Gln	Asn	Val	Asp	Asp	Thr	Leu	
200	65					70					75					80	
202	gcc	ttc	tgg	tcc	aag	cac	gtc	gac	ggg	gac	cag	tgc	ttg	gtc	ttg	ccc	288
203	Ala	Phe	Trp	Ser	Lys	His	Val	Asp	Gly	Asp	Gln	Cys	Leu	Val	Leu	Pro	
204						85				90					95		
206	ttg	gag	cac	ccg	tgc	gcc	agc	ctg	tgc	tgc	ggg	cac	ggc	acg	tgc	atc	336
207	Leu	Glu	His	Pro	Cys	Ala	Ser	Leu	Cys	Cys	Gly	His	Gly	Thr	Cys	Ile	
208				100					105					110			
210	gac	ggc	atc	ggc	agc	ttc	agc	tgc	gac	tgc	cgc	agc	ggc	tgg	gag	ggc	384
211	Asp	Gly	Ile	Gly	Ser	Phe	Ser	Cys	Asp	Cys	Arg	Ser	Gly	Trp	Glu	Gly	
212			115					120					125				
214	cgc	ttc	tgc	cag	cgc	gag	gtg	agc	ttc	ctc	aat	tgc	tcg	ctg	gac	aac	432
215	Arg	Phe	Cys	Gln	Arg	Glu	Val	Ser	Phe	Leu	Asn	Cys	Ser	Leu	Asp	Asn	
216		130				135					140						
218	ggc	ggc	tgc	acg	cat	tac	tgc	cta	gag	gag	gtg	ggc	tgg	cgg	cgc	tgt	480
219	Gly	Gly	Cys	Thr	His	Tyr	Cys	Leu	Glu	Glu	Val	Gly	Trp	Arg	Arg	Cys	
220	145					150					155				160		
222	agc	tgt	gcg	cct	ggc	tac	aag	ctg	ggg	gac	gac	ctc	ctg	cag	tgt	cac	528
223	Ser	Cys	Ala	Pro	Gly	Tyr	Lys	Leu	Gly	Asp	Asp	Leu	Leu	Gln	Cys	His	
224				165						170					175		
226	ccc	gca	gtg	aag	ttc	cct	tgt	ggg	agg	ccc	tgg	aag	cgg	atg	gag	aag	576
227	Pro	Ala	Val	Lys	Phe	Pro	Cys	Gly	Arg	Pro	Trp	Lys	Arg	Met	Glu	Lys	
228				180					185					190			
230	aag	cgc	agt	cac	ctg	aaa	cga	gac	aca	gaa	gac	caa	gaa	gac	caa	gta	624
231	Lys	Arg	Ser	His	Leu	Lys	Arg	Asp	Thr	Glu	Asp	Gln	Glu	Asp	Gln	Val	
232			195					200					205				
234	gat	ccg	cgg	ctc	att	gat	ggg	aag	atg	acc	agg	cgg	gga	gac	agc	ccc	672
235	Asp	Pro	Arg	Leu	Ile	Asp	Gly	Lys	Met	Thr	Arg	Arg	Gly	Asp	Ser	Pro	
236		210				215						220					
238	tgg	cag	gtg	gtc	ctg	ctg	gac	tca	aag	aag	aag	ctg	gcc	tgc	ggg	gca	720
239	Trp	Gln	Val	Val	Leu	Leu	Asp	Ser	Lys	Lys	Lys	Leu	Ala	Cys	Gly	Ala	
240	225				230						235				240		
242	gtg	ctc	atc	cac	ccc	tcc	tgg	gtg	ctg	aca	gcg	gcc	cac	tgc	atg	gat	768
243	Val	Leu	Ile	His	Pro	Ser	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Met	Asp	
244				245						250				255			
246	gag	tcc	aag	aag	ctc	ctt	gtc	agg	ctt	gga	gag	tat	gac	ctg	cgg	cgc	816
247	Glu	Ser	Lys	Lys	Leu	Leu	Val	Arg	Leu	Gly	Glu	Tyr	Asp	Leu	Arg	Arg	
248			260					265					270				
250	tgg	gag	aag	tgg	gag	ctg	gac	ctg	gac	atc	aag	gag	gtc	ttc	gtc	cac	864
251	Trp	Glu	Lys	Trp	Glu	Leu	Asp	Leu	Asp	Ile	Lys	Glu	Val	Phe	Val	His	
252			275					280					285				
254	ccc	aac	tac	agc	aag	agc	acc	acc	gac	aat	gac	atc	gca	ctg	ctg	cac	912
255	Pro	Asn	Tyr	Ser	Lys	Ser	Thr	Thr	Asp	Asn	Asp	Ile	Ala	Leu	Leu	His	
256		290				295						300					
258	ctg	gcc	cag	ccc	gcc	acc	ctc	tcg	cag	acc	ata	gtg	ccc	atc	tgc	ctc	960
259	Leu	Ala	Gln	Pro	Ala	Thr	Leu	Ser	Gln	Thr	Ile	Val	Pro	Ile	Cys	Leu	
260	305					310					315				320		

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262 ccg gac agc ggc ctt gca gag cgc gag ctc aat cag gcc ggc cag gag      1008
263 Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
264          325          330          335
266 acc ctc gtg acg ggc tgg gga tat cac agc agc cga gag aag gag gcc      1056
267 Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
268          340          345          350
270 aag aga aac cgc acc ttc gtc ctc aac ttc atc aag att ccc gtg gtc      1104
271 Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
272          355          360          365
274 ccg cac aat gag tgc agc gag gtc atg agc aac atg gtg tct gag aac      1152
275 Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
276          370          375          380
278 atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc      1200
279 Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
280 385          390          395          400
282 gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg      1248
283 Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
284          405          410          415
286 gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac      1296
287 Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
288          420          425          430
290 ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg att cat ggg cac      1344
291 Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
292          435          440          445
294 atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct taa ctg gaa      1392
295 Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro Leu Glu
296          450          455          460
298 ccc acg tac tgc gac ctc gcc cct ccc gct ggc acg acc gat gcc gct      1440
299 Pro Thr Tyr Cys Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala
300          465          470          475
302 cac cct ggc cgg agc gtc gtg cct gcc ctc ctg cct ctg ctc gcc ggg      1488
303 His Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly
304 480          485          490          495
306 acc ctc ctg ctc ctg gaa acc gct acc gct ccc tagtaatagt ga      1533
307 Thr Leu Leu Leu Leu Glu Thr Ala Thr Ala Pro
308          500          505
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 1533
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial
316 <220> FEATURE:
317 <223> OTHER INFORMATION: PC-UGAC-GPI-4Stop cassette
320 <220> FEATURE:
321 <221> NAME/KEY: exon
322 <222> LOCATION: (1)..(1521)
324 <400> SEQUENCE: 3
325 atg tgg cag ctc aca agc ctc ctg ctg ttc gtg gcc acc tgg gga att      48
326 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
327 1          5          10          15

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/587,804

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Input Set : A:\0279woSEQ.ST25.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date